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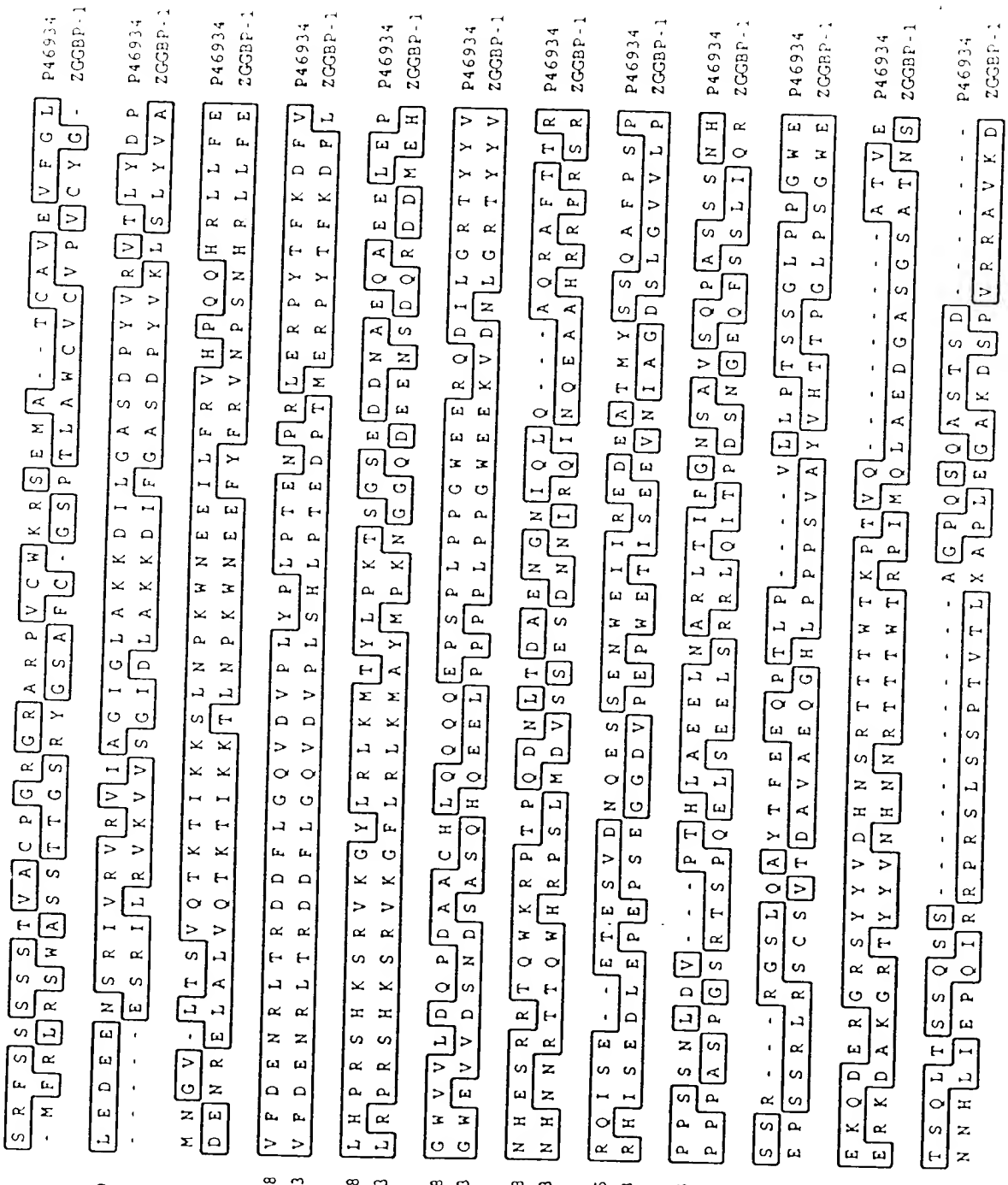

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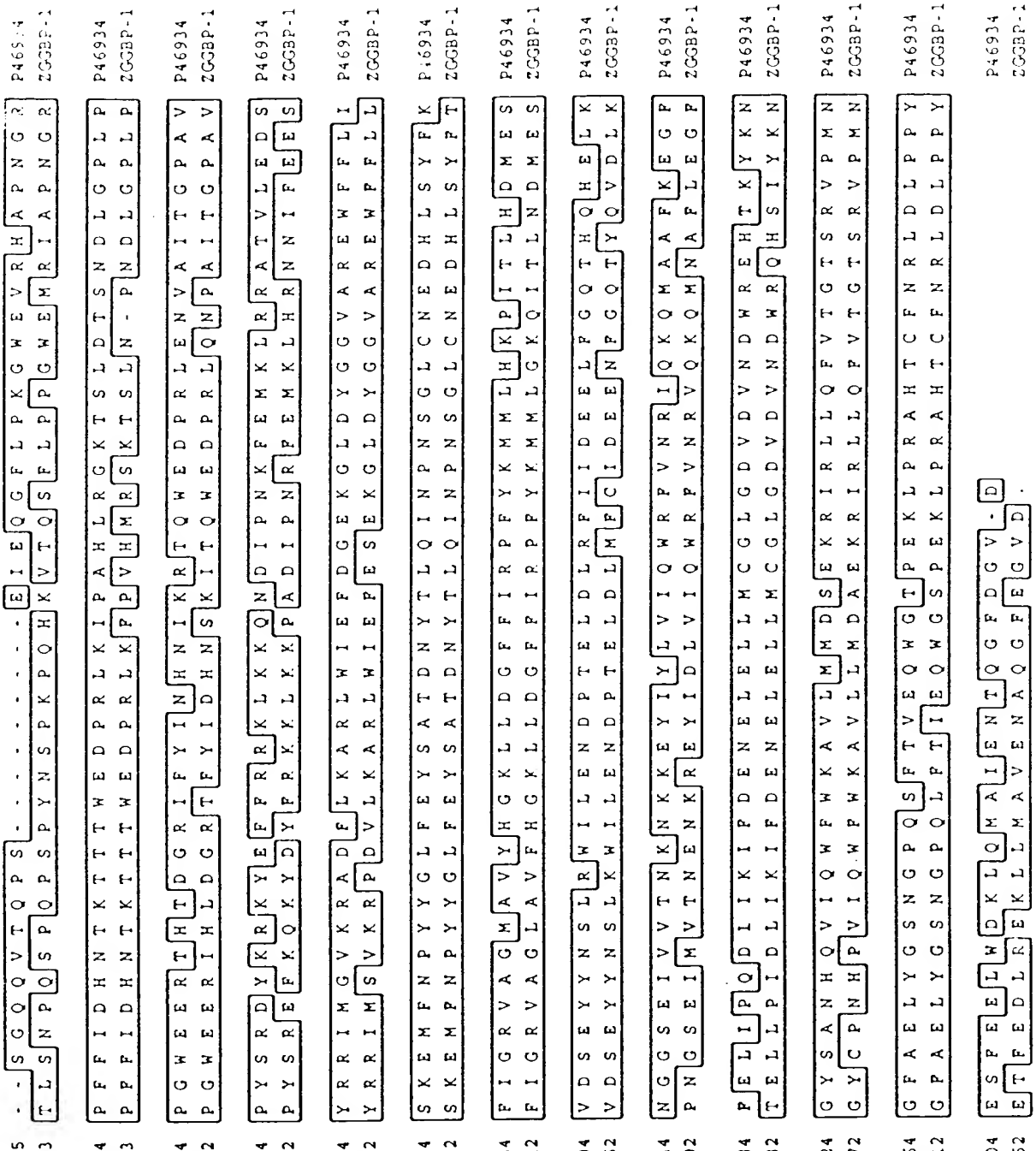

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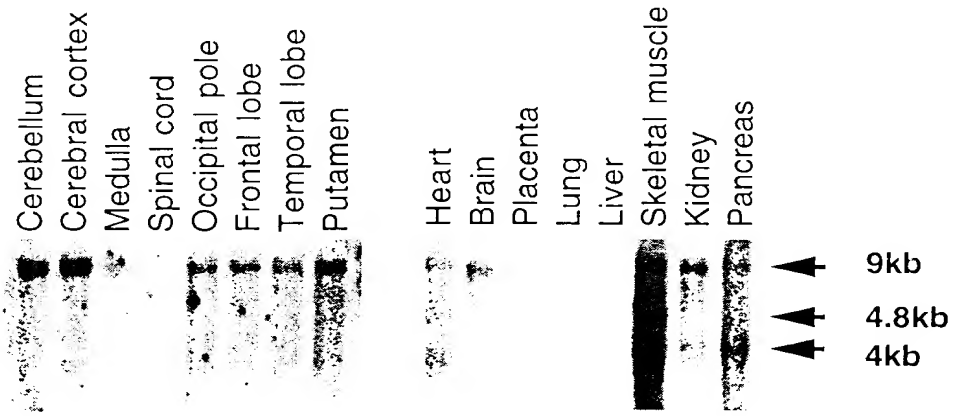
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Figure 4a

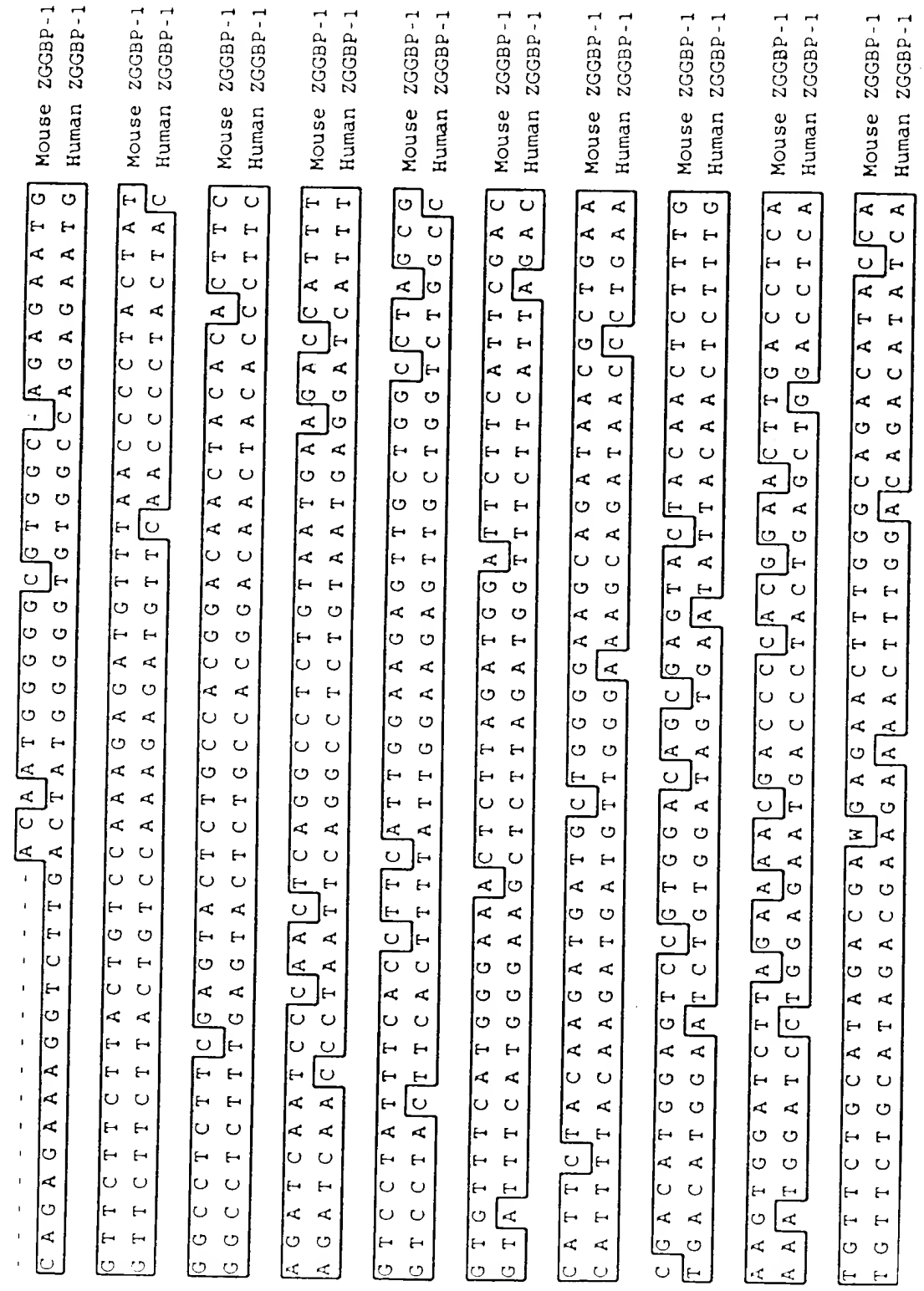
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Figure 4b

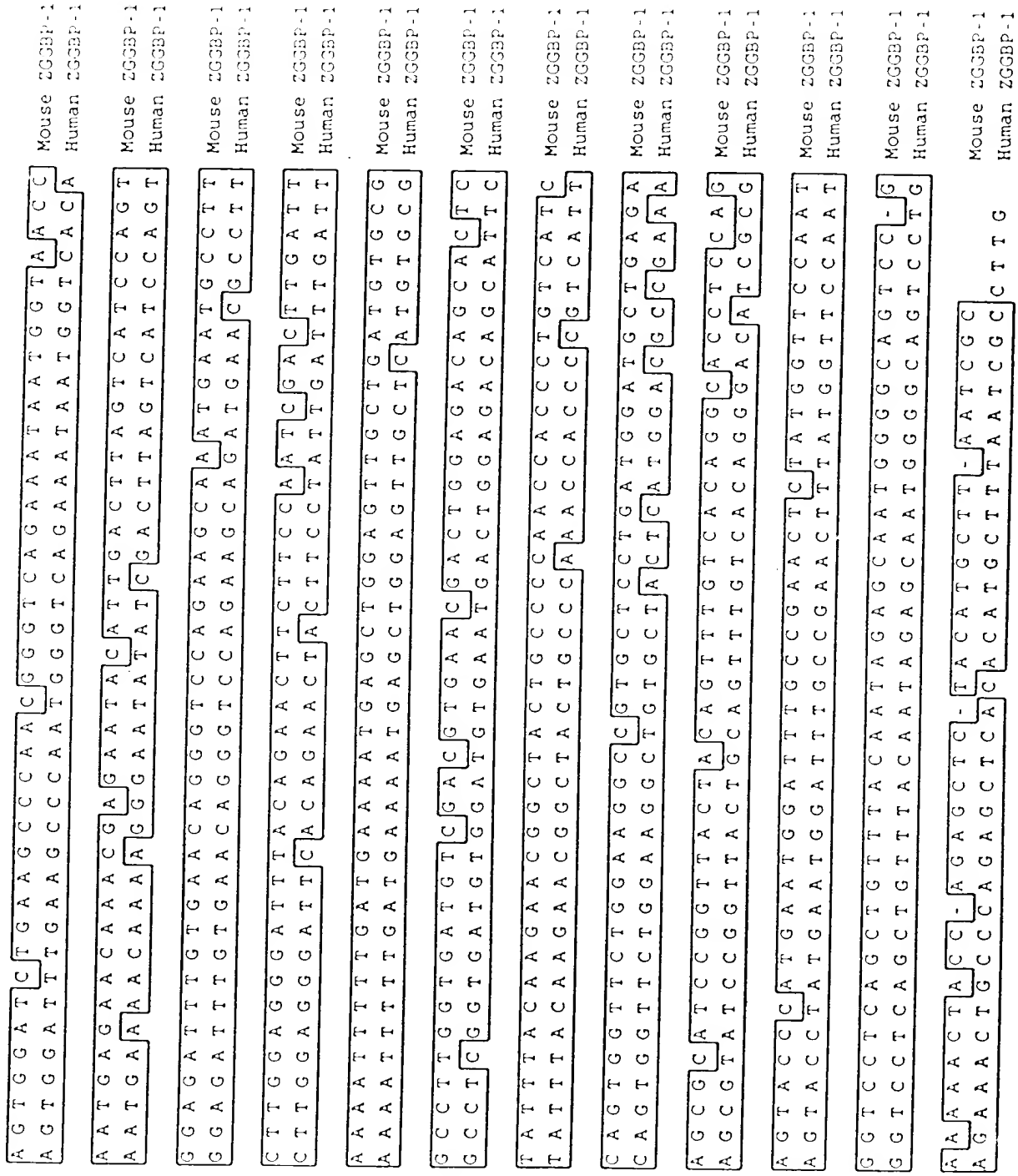
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Figure 5a

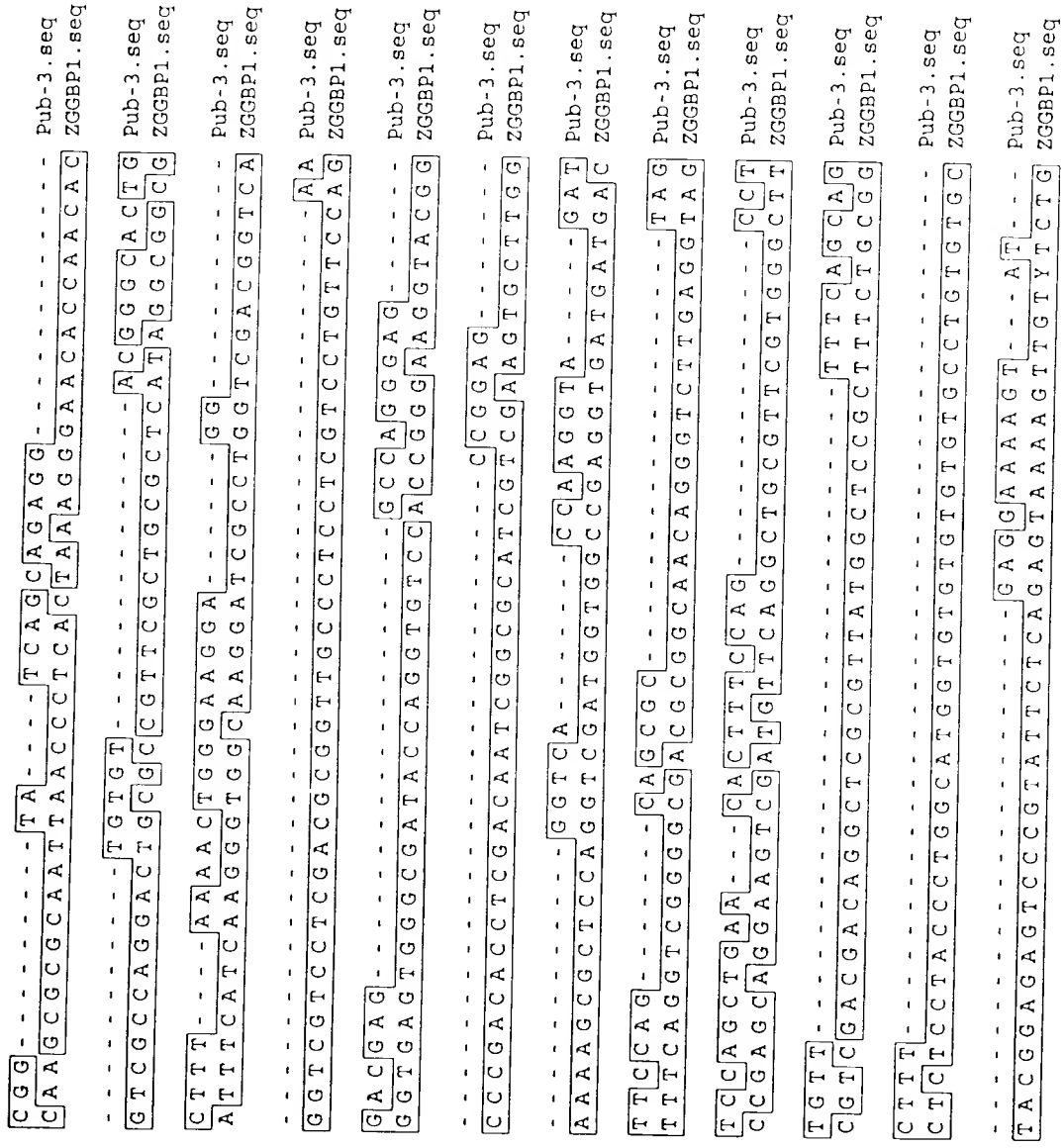
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Figure 5b

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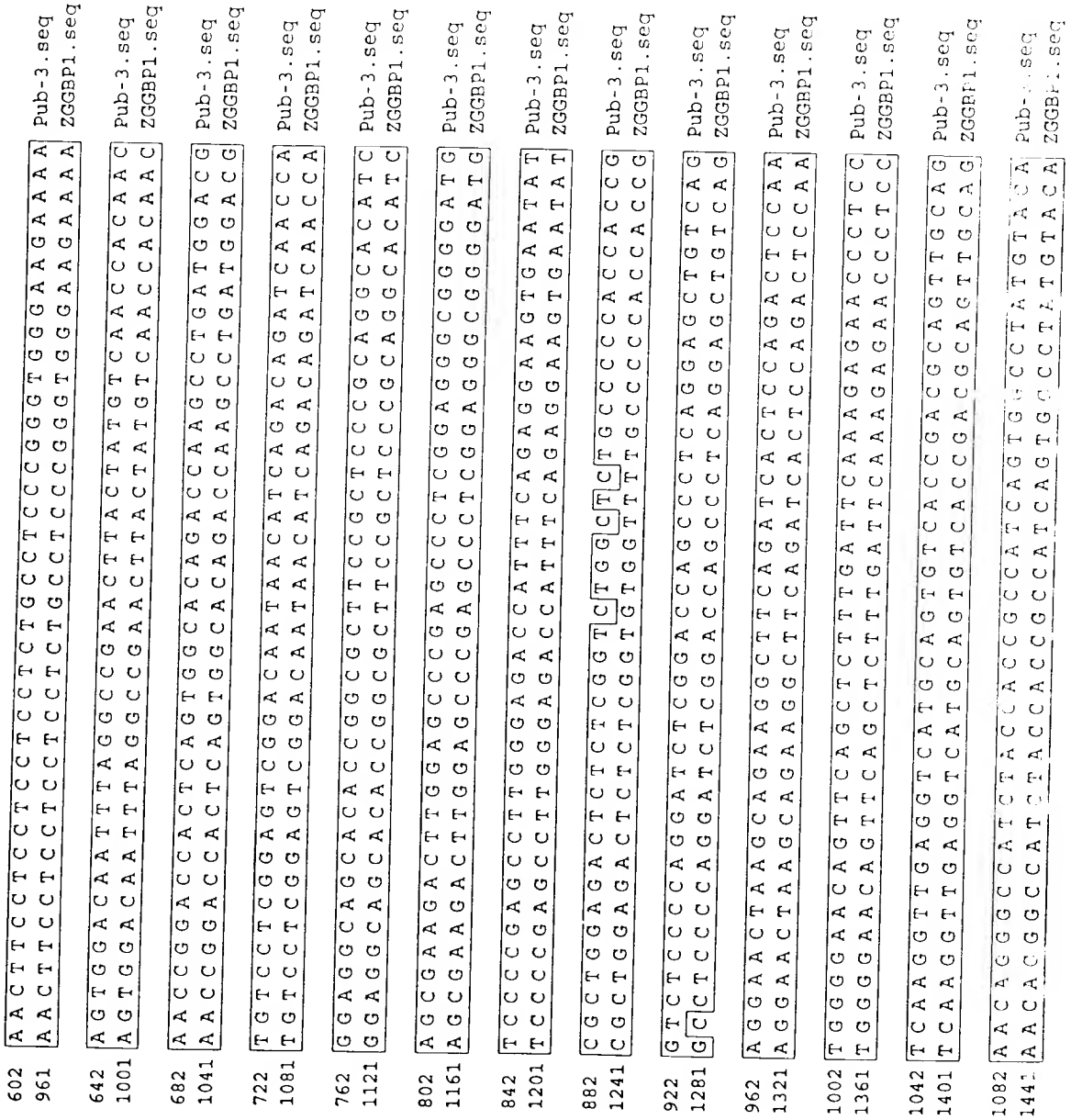
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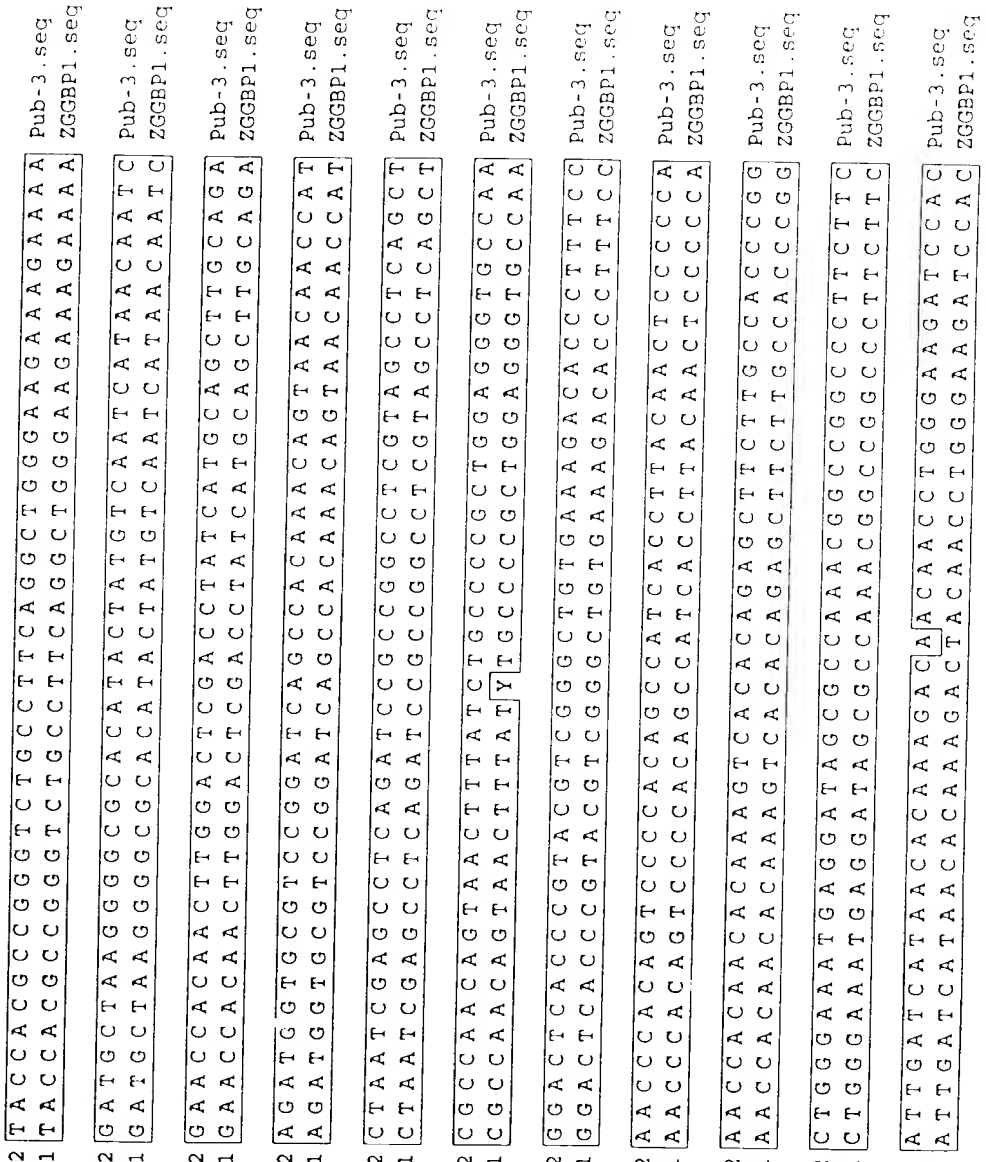
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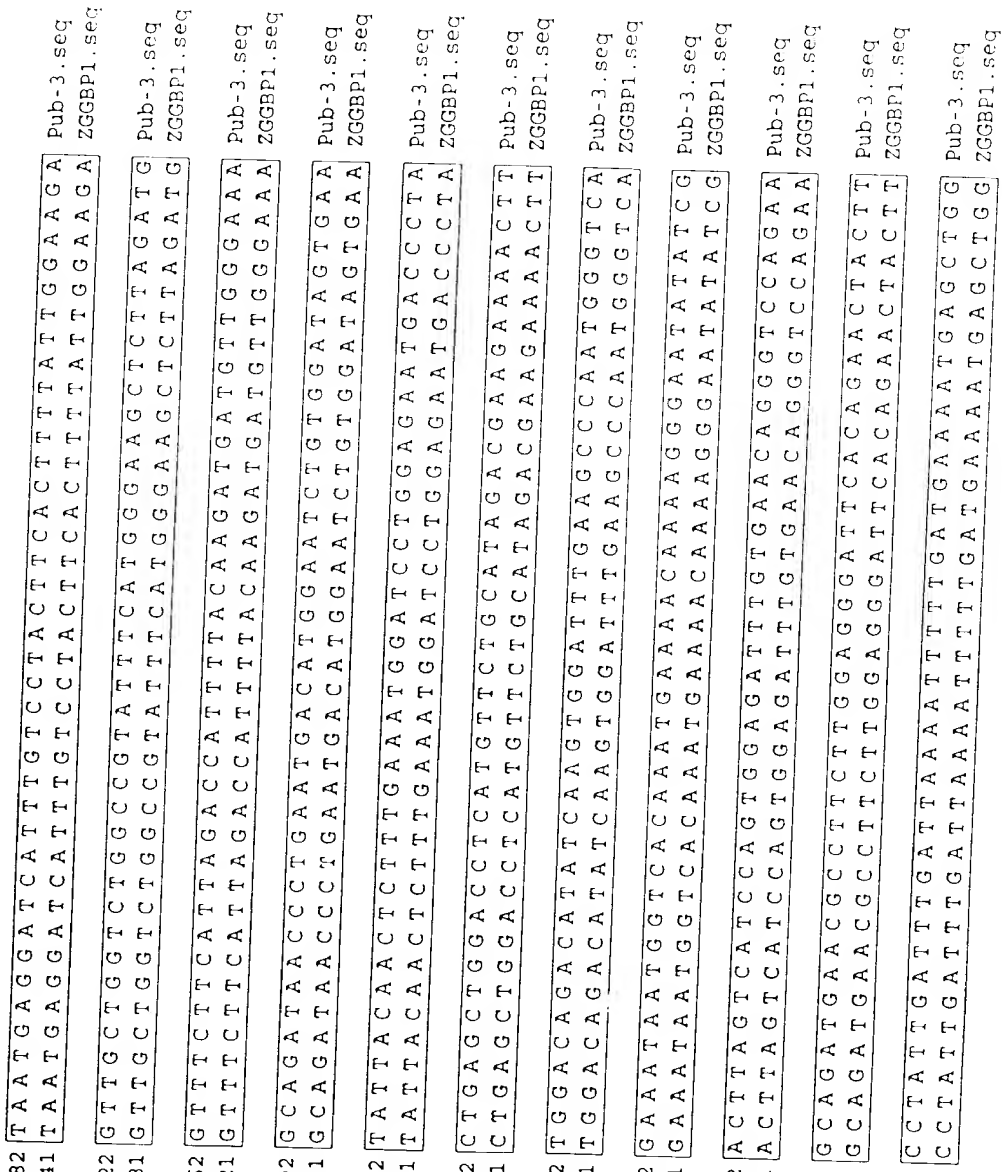
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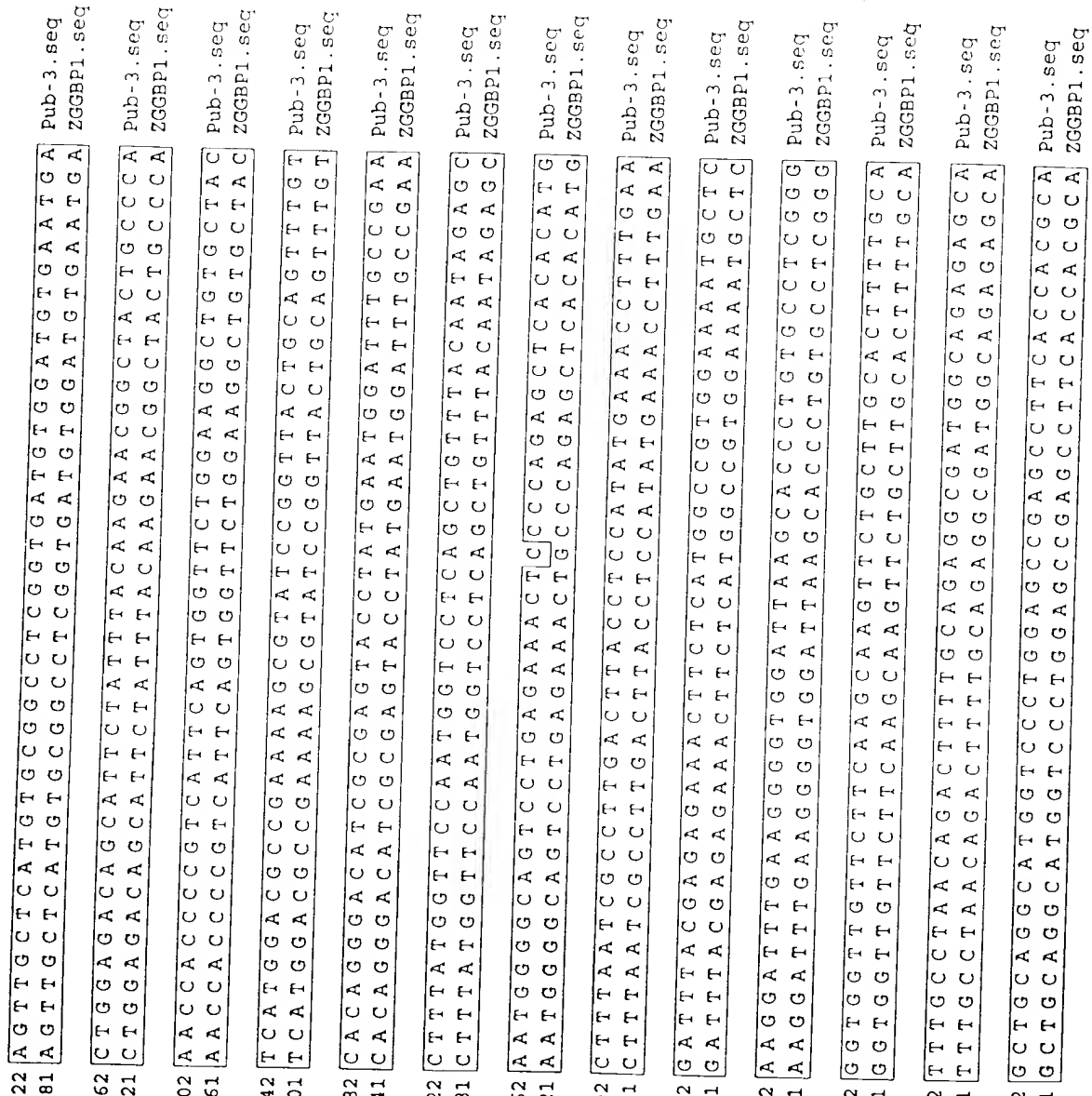
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2842 GATTTACGAGAGAAACTTCTCATGGCCGTGGAAAATGCTC Pub-3.seq
3201 GATTTACGAGAGAAACTTCTCATGGCCGTGGAAAATGCTC ZGGBP1.seq
2882 AAGGATTTGAAGGGGTGGATTAAGCACCCTGTGCCTCGGG Pub-3.seq
3241 AAGGATTTGAAGGGGTGGATTAAGCACCCTGTGCCTCGGG ZGGBP1.seq
2922 GGTGGTTGTTCTTCAAGCAAGTTCTGCTTGCACTTTTGCA Pub-3.seq
3281 GGTGGTTGTTCTTCAAGCAAGTTCTGCTTGCACTTTTGCA ZGGBP1.seq
2962 TTTGCCTAACAGACTTTTGCAGAGGCGATGGCAGAGAGCA Pub-3.seq
3321 TTTGCCTAACAGACTTTTGCAGAGGCGATGGCAGAGAGCA ZGGBP1.seq
3002 GCTGCAGGCATGGTCCCTGGAGCCGAGCCTTCACCACGCA Pub-3.seq
3361 GCTGCAGGCATGGTCCCTGGAGCCGAGCCTTCACCACGCA ZGGBP1.seq

Figure 5h

```
3208 ---------------------------------------- Pub-3.seq
3840 AGACAAGTACTTTGAGAGAATTTCCAATATAATATTAGAC ZGGBP1.seq

3208 -----------------------------AAAAAA----- Pub-3.seq
3880 ATAATGATAATTTTTTCCATACTCAGAATGAAAAACTGGA ZGGBP1.seq

3214 ---------------------------------------- Pub-3.seq
3920 TATTACGTTTTTGTTTTGGGTTTTTTTGTACAAATTTAG ZGGBP1.seq

3214 ---------------------------------------- Pub-3.seq
3960 CTAATAGCTACAGGCTGAGAGAATTGTAACATAGCATGAC ZGGBP1.seq

3214 ---------------------------------------- Pub-3.seq
4000 AAATTTTGTGTTGACTTGAAAGGAATCACACCATTATTCC ZGGBP1.seq

3214 ---------------------------------------- Pub-3.seq
4040 TTAGAAGTAATTACATGTGTTCTAACACATTTGAGACAGG ZGGBP1.seq

3214 ---------------------------------------- Pub-3.seq
4080 GTTGGACTCCCATTTCTCATCCGAGAAATTACTTAACCCT ZGGBP1.seq

3214 ---------------------------------------- Pub-3.seq
4120 TCCTGGGCGCTGTACAGTCATCTTTTATTCTATTTCCTCT ZGGBP1.seq

3214 ---------------------------------------- Pub-3.seq
4160 TTGCTGTTTGTAGTAGAGACATTTTGAATGAAACTTGGCA ZGGBP1.seq

3214 ---------------------------------------- Pub-3.seq
4200 CTGCTTGATTCAAAACTGTGGAAACCAGATCTGTTTAGTC ZGGBP1.seq

3214 ---------------------------------------- Pub-3.seq
4240 TCCTGTTTGTATGCGTTTGCTAATGGTAGCTAAATAACCA ZGGBP1.seq

3214 ---------------------------------------- Pub-3.seq
4280 GTTTTTGTTGTAAATGCACCAATTCTGAAGGCACTTTATG ZGGBP1.seq

3214 ---------------------------------------- Pub-3.seq
4320 TACTACATGGAGGTCATATCTGGTTTTGTTTTTATTTTTT ZGGBP1.seq
```

Figure 5i

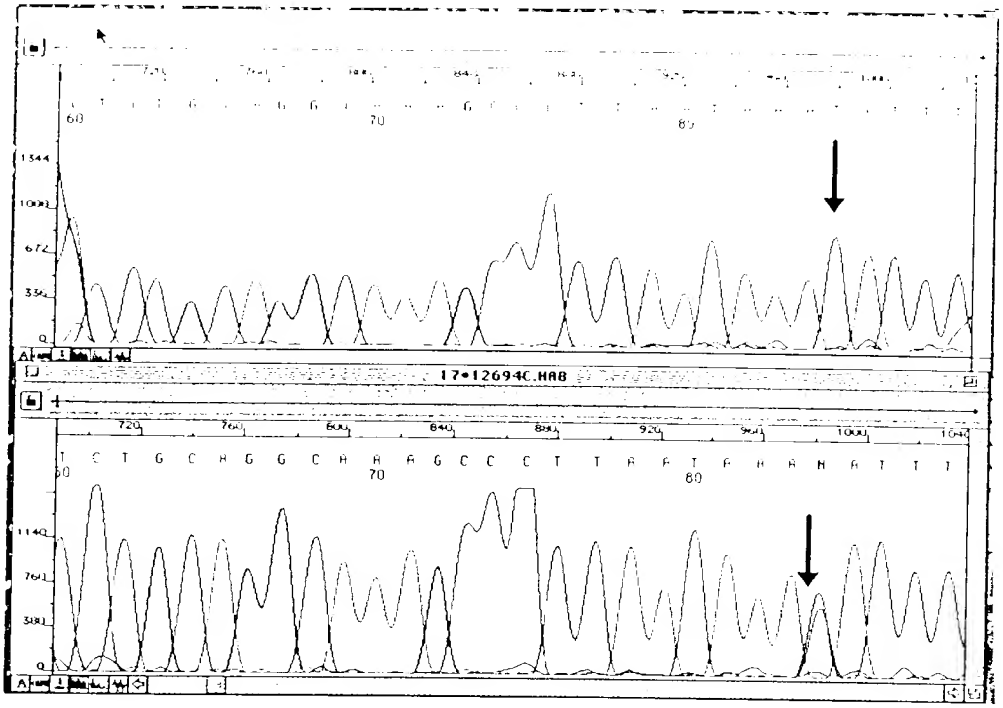
```
3214 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  Pub-3.seq
4360 T A T C A T G A A C A T T A A A T G T G A T G A T G A T T T C T T T T C C C T G  ZGGBP1.seq

3214 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  Pub-3.seq
4400 C A C A C A T C T T T C C G G T G C A A T A T C T A T C A A T T G T G A A T C T  ZGGBP1.seq

3214 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  Pub-3.seq
4440 G G C T G C T G G T G T A T A A A A A C C T G G A T G T A A A G C T G A G C C T  ZGGBP1.seq

3214 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  Pub-3.seq
4480 A C A G A C C T G T C C T C A C C A A C T G T T T T G T G A T T T C T A C T C A  ZGGBP1.seq

3214 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  Pub-3.seq
4520 A C T A C A A A G A T T T A T T T A A T G T A C T C T T A A T C T A A C T G A G  ZGGBP1.seq

3214 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  Pub-3.seq
4560 T T T T G T T A C C A A T G A C C T G T T G C A T G C T T C A A T A C C G T G T  ZGGBP1.seq

3214 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  Pub-3.seq
4600 A C T G C C T G A G T T G T G C C T C T T G T G T G C T A G A T T A A A A G T G  ZGGBP1.seq

3214 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  Pub-3.seq
4640 A G A C A G A G A C T T G A C T T G A T C C T C T G A G C C T C A A G C T A T T  ZGGBP1.seq

3214 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  Pub-3.seq
4680 G A G C T G G T A G T G G C A G A G G A C T G A G G G T A C C T G C A C A G T T  ZGGBP1.seq

3214 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  Pub-3.seq
4720 T G A T T C T T T T C C C A C G T T G T A A G T C T C C A T T G C A G A A T T G  ZGGBP1.seq

3214 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  Pub-3.seq
4760 T C G T G C G T T T G A G A A A A C A C C T G A G G C A G T G T G G G A G T T G  ZGGBP1.seq
```

Figure 5j

```
3214 ----------------------------------------  Pub-3.seq
4800 AACGACCCTGCTGTCCTTTTTAACCTGTGTTGTCCTAGAC  ZGGBP1.seq

3214 ----------------------------------------  Pub-3.seq
4840 CTGTCGGGGCAGTCAGGGGACACTAGAGATTTGATCTCAT  ZGGBP1.seq

3214 ------------------AAAAAA----------------  Pub-3.seq
4880 GCGAGTCATCAATAGGACAAAAAAGTTGTGGTTTGGGGAG  ZGGBP1.seq

3220 ----------------------------------------  Pub-3.seq
4920 GTCTGTTTGTTACATAAAAAGGACCTTTCGGTGTAAGAAA  ZGGBP1.seq

3220 ----------------------------------------  Pub-3.seq
4960 TTGCCGTTTTTACCCTGCCCTGGCTGGCATGTGAGAAGCC  ZGGBP1.seq

3220 ----------------------------------------  Pub-3.seq
5000 ATGGAAGGTTGTGGTTGTAAATGAGTTGTCTAAAGGGGTG  ZGGBP1.seq

3220 ------------------AAAAAAA                 Pub-3.seq
5040 CAGAGGCCTGAGGTTTCTAAAAGAAGGTAGATTTCTACAG  ZGGBP1.seq

3226                                           Pub-3.seq
5080 AGCTGA[illegible]TGTTGGTTCCTTTTTCTTATTGGTTGAAAATTA  ZGGBP1.seq

3226                                           Pub-3.seq
5120 CCTGGTAGTGATCAGAAAACTTAGATGCTATGTAACTC    ZGGBP1.seq
```

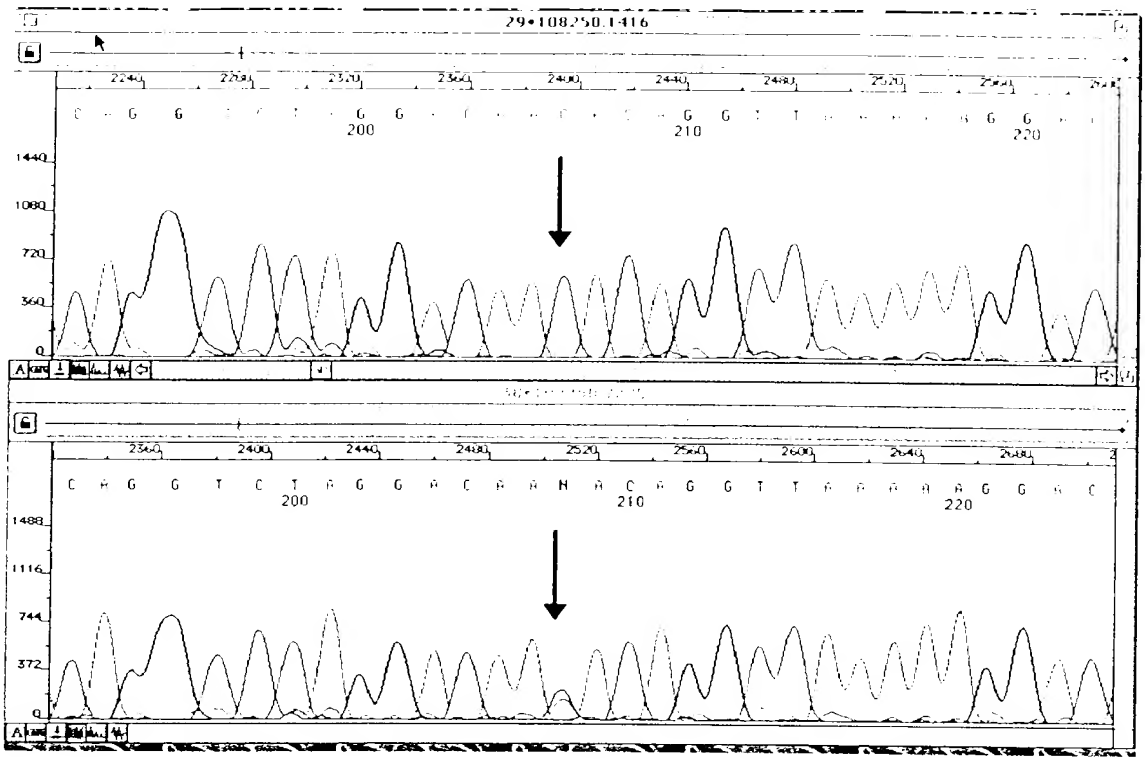
Decoration 'Decoration #1': Box residues that match the Consensus exactly.

Figure 6



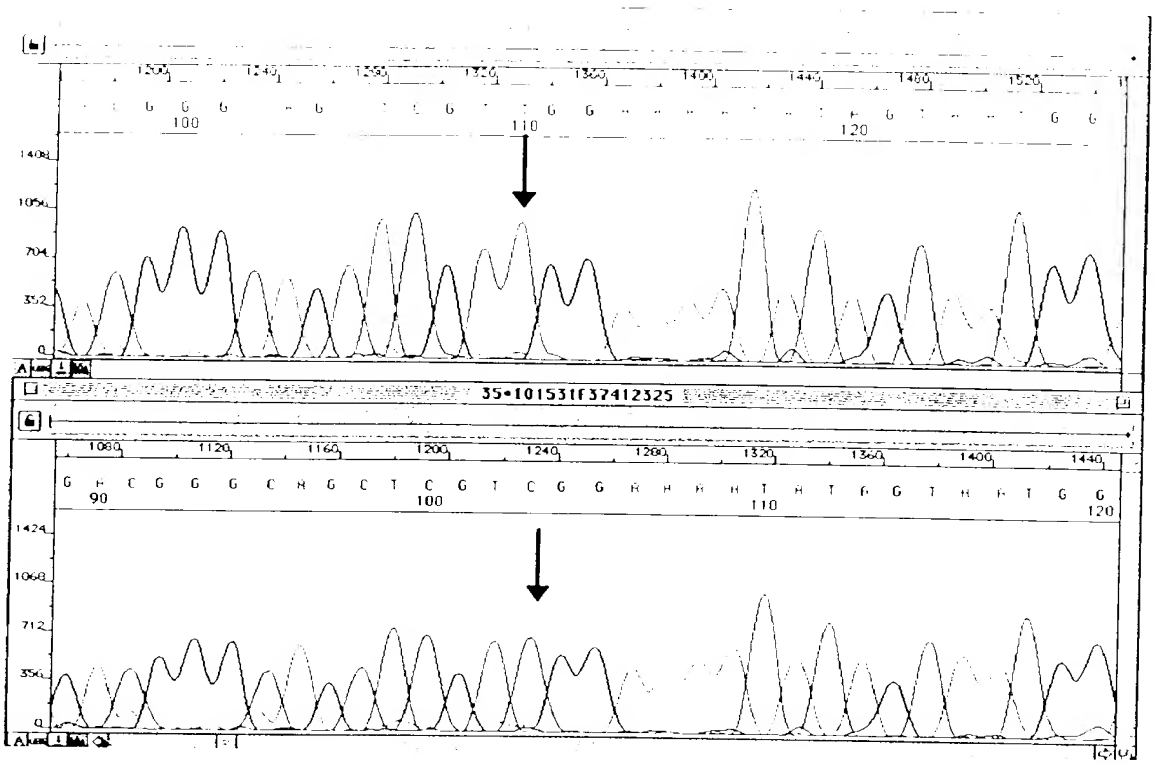
Wild Type (human foetal brain)	**T/T**
Variant Type (human adult brain)	**T/C**
Polymorphism Position	**3554**
RFLP	**-**

Figure 7



Wild Type (GM1416)	C/C
Variant (7225)	C/G
Position	4828

Figure 8



Primer sequences derived from BAC and used on lymphoblastoid cell lines from BPAD Patients.

Homozygous wild type (KK169) - T/T

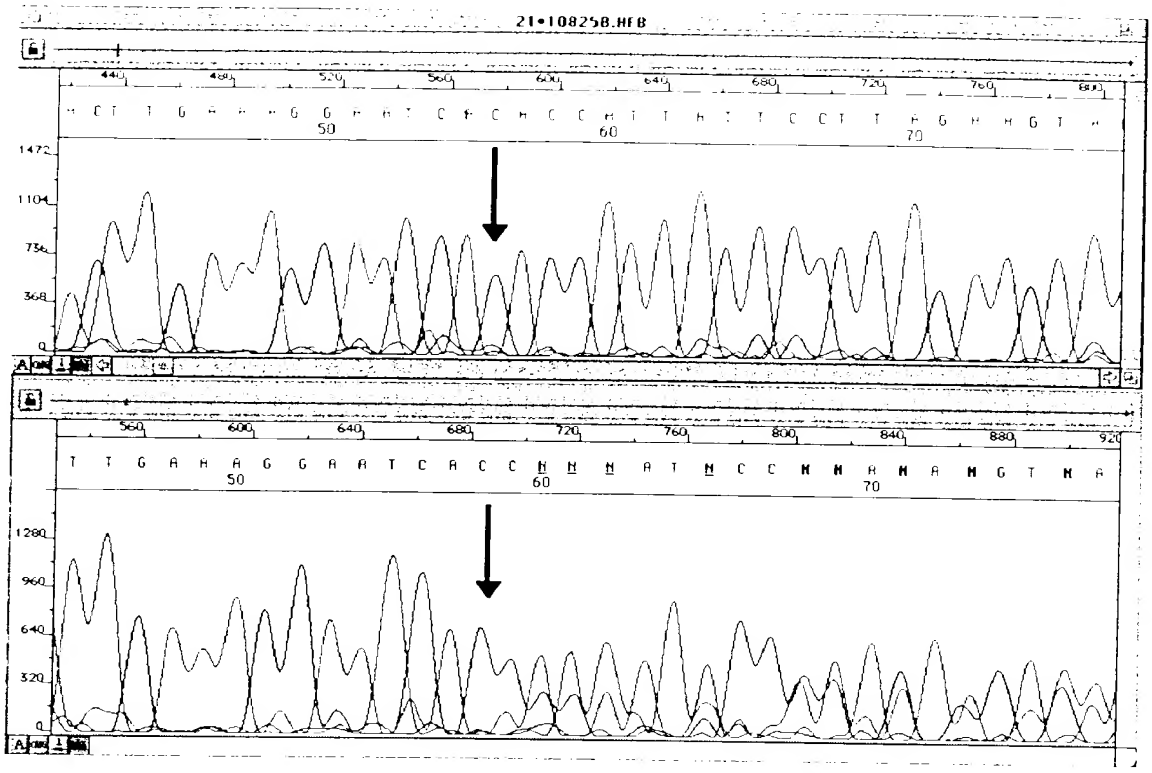
Homozygous variant (KK232) - C/C

Figure 9

TGCTGCAAGTGACAGGTTCCAAGAAGCCCGAGGGCTCAGAGCTGAATGATGAAGCGC
AGTCCCCAAAGTGCCTGGCCACCCCTCCCTCCCTGGATCACTGCTGCCTGGGCTTGA
TTGATTGATTGATTGATTGATTGATTGATTTTGAGAGAGATTCTCACTGTCACCCAG
GCTGGAGTACAGTGGTGCGATCTCGGCTCACTGCAGCCTCTGCCTCCCGGGTTCAAG
CAATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTACAGGCACGCGCCACCACAC
CCAGCTAATTTTGTATTTTTAGTAAAAGACGGGGTTTCACCATGTTGGGCCAGGATG
GTCTTGATCTCCTGACCTCATGATCCACCCGCCCCGGCTTCCAAAGTGCTGGGATAC
AGGCATGAACCCGACGCGCCCAGCATGGACATTTTTTTTTAATCCCCTGCCCTTTTC
TTGNGGCATAATTCATTGCAGGTCTCTTCTATACAGATCATGGAAAACACATTTTCT
TAACTGAGTTNTTATTATTTATACCCAGNCACCTCATGACANNTTTACCCTGTTACA
NACAAAATGGGCACCTGCCAAAANCAACTTTNATATAAGGATGCTCCAGGCCT

Tetranucleotide repeat underlined

Figure 10



Top electropherogram (human foetal brain) - wild type

Lower electropherogram (7225) - heterozygous variant

Arrow indicates the position of the C+C insertion - position 4032